RAW SEQUENCE LISTING ERROR REPORT
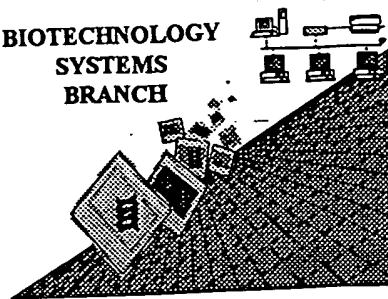
BIOTECHNOLOGY SYSTEMS BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/605,573_

Source: _OIPE_

Date Processed by STIC: _7/12/2000_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,

2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

<u>Checker Version 3.0 can be down loaded from the USPTO website at the following address:</u>
http://www.uspto.gov/web/offices/pac/checker

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/605,573

DATE: 07/12/2000
TIME: 11:03:21

Input Set : A:\CDS222 Listing for disk.txt
Output Set: N:\CRF3\07122000\I605573.raw

Does Not Comply Corrected Diskette Needed

```
      3 <110> APPLICANT: De Leys, Robert J.
      4        Zheng, Jian
      6 <120> TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
      8 <130> FILE REFERENCE: CDS-207
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/605,573
C--> 11 <141> CURRENT FILING DATE: 2000-06-28
E--> 13 <160> NUMBER OF SEQ ID NOS: 69 —770 (next page)
     15 <170> SOFTWARE: PatentIn Ver. 2.0
```

ERRORED SEQUENCES

FYI

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.

BEST AVAILABLE COPY

7/12/00

VERIFICATION SUMMARY   DATE: 07/12/2000
PATENT APPLICATION: US/09/605,573   TIME: 11:03:22

Input Set : A:\CDS222 Listing for disk.txt
Output Set: N:\CRF3\07122000\I605573.raw

```
L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1080 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:60
L:1080 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:60
L:1080 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:60
L:1114 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:62
L:1114 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:62
L:1114 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:62
L:1131 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:63
L:1131 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:63
L:1131 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:63
L:1148 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:64
L:1148 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:64
L:1148 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:64
L:13 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (69) Counted (70)
```

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